

FIGURE 1A

| | | | | | | | | | | |
|------|------------|-------------|------------|-------------|-------------|-------------|------------|------------|-------------|--------------|
| 1 | GNTCTAGAA | TAGTGGATCC | CCCCGGGCTG | CAGGAATTCC | GACGGCCCTT | GGAAGGGCTC | TGGTGGGGCT | GAGCGCTCTG | CCGCGGGGGC | GCGGCACAG |
| | CNAGATCTTN | ATCACCTAGG | GGGGCCCGAC | GTCTTAAGG | CTGCCGGGA | CCTTCCCGAG | ACCACCCCGA | CTCGCGAGAC | GGCGCCCGCG | CGCCCGTGTC |
| 101 | CAGGAAGCAG | GTCCCGCTGG | CGCTGGGGG | CATCAGCTAC | CGGGTGCTC | CGGGCTGAAG | AGCCAGGCAG | CCAAGGCAGC | CACCCCGGGG | GGTGGGCGAC |
| | GTCTCTCGTC | CAGGCGCACC | CGCGACCCCG | GATGTCGATG | GCCCCACCCAG | GCCCGACTTC | TGGTCCGTC | GGTTCGTCG | GTGGGGCCCC | CCACCCGCTG |
| 201 | TTTGGGGGAG | TTGGTGCCCG | GCCCCCAGG | CCTTGGCGGG | GTCTATGGGC | CCCCCATTC | TGGGCGGGG | GCGTGGCGAG | TCCGGGGCCCT | GCTGTGCTG |
| | AAACCCCTC | AACCACGGG | CGGGGGTCC | GGAACCGCCC | CAGTACCCCG | GGGGGGTAAG | ACCCGGCCCC | CCGCACGCTC | AGCCCCGGGA | CGACGACGAC |
| 1 | | | | | MetGlyP | roProHisSe | rGlyProGly | GlyValArgV | alGlyAlaLe | uLeuLeuLeu |
| 301 | GGGGTTTGG | GGCTGGTGT | TGGGCTCAGC | CTGGAGCCTG | TCTACTGGAA | CTCGGCGAAT | AAGAGGTTC | AGGCAGAGGG | TGGTTATGTG | CTGTACCCCTC |
| | CCCCAAAACC | CCGACCACAG | ACCCGAGTCG | GACCTCGGAC | AGATGACCTT | GAGCCGCTTA | TTCGCAAGG | TCCGTCTCCC | ACCAATACAC | GACATGGGAG |
| 401 | GlyValLeuG | lyLeuValSe | rGlyLeuSer | LeuGluProV | alTyrTrpAs | nSerAlaAsn | LysArgPheG | InAlaGluG | yGlyTyrVal | LeuTyrProGln |
| 54 | IleGlyAs | pArgLeuAsp | LeuLeuCysP | roArgAlaAr | gProProGly | ProHisSerS | erProAsnTy | rGluPheTyr | LysLeuTyrL | euValGlyGly |
| 501 | TGCTCAGGGC | CGGCGCTGTG | AGGCACCCCG | TGCCCCAAAC | CTCCTTCTCA | CTTGTGATCG | CCAGACCTG | GATCTCCGCT | TCACCATCAA | GTTCACAGGAG |
| | ACGAGTCCCG | GCCGCGACAC | TCCGTGGGG | ACGGGGTTTG | GAGGAAGAGT | GAACACTAGC | GGGTCTGGAC | CTAGAGGCGA | AGTGGTAGTT | CAAGGTCTCTC |
| 87 | AlaGlnGly | ArgArgCysG | luAlaProPr | oAlaProAsn | LeuLeuLeuT | hrCysAspAr | gProAspLeu | AspLeuArgP | heThrIleLy | sPheGlnGlu |
| 601 | TATAGCCCTA | ATCTCTGGGG | CCACGAGTTC | CGCTCGCACC | ACGATTACTA | CATCATTTGCC | ACATCGGATG | GGACCCGGGA | GGGCTGGAG | AGCCTGCAGG |
| | ATATCGGGAT | TAGAGACCCC | GGTCTCAAG | GCGAGCGTGG | TGCTAATGAT | GTAGTAACGG | TGTAGCCTAC | CCTGGGCCCT | CCCGACCTC | TCCGACGTCC |
| 120 | TyrSerProA | snLeuTrpGl | yHisGluPhe | ArgSerHisH | isAspTyrTy | rIleIleAla | ThrSerAspG | lyThrArgG | uGlyLeuGlu | SerLeuGlnGly |
| 701 | GAGGTGTGTG | CCTAACACAG | GGCATGAAGG | TGCTTCTCCG | AGTGGGACAA | AGTCCCGCAG | GAGGGGCTGT | CCCCCGAAAA | CCTGTGTCTG | AAATGCCCAT |
| | CTCCACACAC | GGATTGTCT | CCGTACTTCC | ACGAAGAGGC | TCACCCTGTT | TCAGGGGCTC | CTCCCCGACA | GGGGGCTTTT | GGACACAGAC | TTTACGGGTA |
| 154 | GlyValCy | sLeuThrArg | GlyMetLysV | alLeuLeuAr | gValGlyGln | SerProArgG | lyGlyAlaVa | lProArgLys | ProValSerG | luMetProMet |
| 187 | GGAAAGAGAC | CGAGGGGCAG | CCCACAGCCT | GGAGCCTGGG | AAGGAGAACC | TGCCAGGTGA | CCCCACCAGC | AATGCAACCT | CCCGGGGTGC | TGAAGGCCCC |
| | CCTTTCTCTG | GCTCCCCGTC | GGGTGTGGA | CCTCGACCC | TTCCTCTTGG | ACGGTCCACT | GGGGTGGTCG | TTACGTTTGA | GGGCCCCACG | ACTTCCGGGG |
| 187 | GluArgAsp | ArgGlyAlaA | laHisSerLe | uGluProGly | LysGluAsnL | euProGlyAs | pProThrSer | AsnAlaThrS | erArgGlyAl | aGluGlyPro |
| 901 | CTGCCCCCTC | CCAGCATGCC | TGCAGTGGCT | GGGCGACGAG | GGGGGCTGGC | GCTGCTCTTG | CTGGGCGTGG | CAGGGGCTGG | GGGTGCCATG | TGTTGGCGGA |
| | GACGGGGGAG | GSTCGTACGG | ACGTACCCGA | CCCCCGTCTC | CCCCCGACCG | CGACGAGAAC | GACCCGACCC | GTCCCCGACC | CCCACGGTAC | ACAAACCGCT |
| 220 | LeuProProp | roSerMetPr | oAlaValAla | GlyAlaAlaG | lyGlyLeuAl | aLeuLeuLeu | LeuGlyVala | laGlyAlaGl | yGlyAlaMet | CysTrpArgArg |
| 1001 | GACGGCGGGC | CAAGCCTTCG | GAGAGTCGCC | ACCCCTGGTCC | TGGTCTCTTC | GGGAGGGGAG | GGTCTCTGGG | CCTGGGGGGT | GGAGGTGGGA | TGGGACCTCG |
| | CTGCCCGCCG | GTTTCGGAAGC | CTCTCAGCG | TGGGACCCAG | ACCGAGGAAG | CCCTCCCTTC | CCAGAGACCC | GGACCCCTCA | CCTCCACCTC | ACCTGGGAGC |
| 254 | ArgArgAl | alysProSer | GluSerArgH | isProGlyPr | oglySerPhe | GlyArgGlyG | lySerLeuG | yLeuGlyGly | GlyGlyGlyM | etGlyProArg |
| 1101 | GGAGGCTGAG | CCTGGGGGAG | TAGGATAGC | TCTCGGGGGT | GGCGGGGCTG | CAGATCCCCC | CTTCTGCCCC | CAGTATGAGA | AGGTAGTGG | TGACTATGGG |
| | CCTCCGACTC | GGACCCCTCG | ATCCCTATCG | AGACGCCCCA | CCGCCCCGAC | GTCATAGGGG | GAAGACGGGG | GTACTACTCT | TCCACTCACC | ACTGATACCC |
| 287 | GluAlaGlu | ProGlyGluL | euGlyIleAl | aleuArgGly | GlyGlyAlaA | laAspProPr | opheCysPro | HisTyrGluL | ysValSerG | lAspTyrGly |

FIGURE 1B

1201 CATCTCTGT ATATCGTGCA GGATGGGCCC CCCAGAGCC CTCAAACAT CTACTACACA TCGATTTCGT TGTGGAGTG GCCATATTG CATACGATAC
GTAGGACACA TATAGCACGT CCTACCCGG GGGTCTCGG GAGTTTGTGAT GATGATGTGT AGCTAAAGAC ACAACCTCAC CGGTATAAC GATGCTATG
320 HisProValT yrIleValG1 nAspGlyPro ProGlnSerP roProAsnI1 eYrTyThr SerIleSerV alLeuGluTr pProIleLeu HisThrIleGln
1301 AACTGTTTTT CATGCGATCC AAGTGCTCCC GTGTCACACTAC ATTCTTATTT CCTGTGCAAG TTATTACGAC ATCGACTTGC CGGATGACTT CATTTAGCTT
TTGACAAAA GTACGCTAGG TTCACGAGGG CACAGTGATG TAAGAATAAA GGACACGTTT AATAATGCTG TAGCTGAACG GCCTACTGAA GTAAATCGAA
354 LeuPhePh eMetArgSer LysCysSerA rgValThrTh rPheLeuPhe ProValGlnV alIleThrTh rSerThrCys ArgMetThrS erPheSerPhe
1401 TACCACCCCTG AACCCATCCA TGCAGGCCCTG CAGAGCACAG ATGGGGGAAT TCCGAATCAG ATGGTGTTC TGGGGGACACA GGATCCTGGG TACGGCTCTG
ATGGTGGGAC TTGGGTAGGT ACGTCCGGAC GTCTCGTGTG TACCCCTTA AGGCTTAGTC TACCACAAAAG ACCCCCTGT CCTAGGACCC ATGCCGAGAC
387 ThrThrLeu AsnProSerM etGlnAlaCy sArgAlaGln MetGlyGluP heArgIleAr gTrpCysPhe TrpGlyAspA rgIleLeuG1 yThrAlaLeu
401 TTTGTGCTTG TGCTTATTCT TCTTCTTGGG AGGCTGAATA TGCATCAGAC GACACTGCTC CGGCAACGGG CCAGTGTGGA GGCGGAAGCC GGCCAGCATG
AAACACGAAC ACGAATAAGA AGAAGAACC TCCGACTTAT ACGTAGTCTG CTGTGACGAG GCCGTTGCC GGTACACACT CCGCTTCGG CCGTTCGTAC
420 PheValLeuV alLeuIleLe uLeuLeuGly ArgLeuAsnM etHisGlnTh rThrLeuLeu ArgGlnArgA laSerValG1 uAlaGluAla GlyGlnHisGly
1601 GTCCCCCTGT ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG GAGGCTGCTG TTATCATGGG AACGAGGCAG ATCAATCATC
CAGGGGACAC TATCCTAACT TTCTCGATGA CTCTTATCCC CCGAAGAGTT ACTCTCTCGC CTCCGACGAC AATAGTACCC TTGGTCCGTC TAGTTAGTAG
454 ProLeu
1701 CCTGGCAGGT CAGGCAGGAA GTTACTTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAAATTA TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCTG
GGACCGTCCA GTCCGTCCTT CAATGAATCG AAGAGGAAGT GGAAGAAGGG TGCTCTAAAT AATATCCGAA CAAGGTTCAA CATCACACAC TAGTCTAAGC
1801 TGCTGCCCTGT CAGCTCTGTG CTACCTGGCA GTTCCCTTCA TGGAAATTCGA TATCAAGCTT ATCGATACCG TCGACCT
ACGACGGACA GTCGAGACAC GATGGACCGT CAAGGGGAGT ACCTTAAGCT ATAGTTCGAA TAGCTATGGC AGCTGGA

FIGURE 2A

1 GNTCTAGAA TACTGCATCC CCCCAGGCTG CAGCAATTCC GACCCGCCCTT CCAAGGGCTC TGCTGGGGCT GAGGGCTCTG CCCCCTGGCC GCGGGGACAC
 CNAATCTTN ATCAGCTAGG GCGGCCCCAC GTCTTTAGG CTGCGGGGA CCTTCTCGAG ACCACCCGA CTCCGAGAC GCGGCCCCCG GCGCCGTGTC
 101 CAGCAACCA CTTCCGCTGG GCGCTGGGG CATCAGCTAC CCGCTGCTC CCGCTGAAG ACCCAGGCAG CCACUUCUGG GCTGGGGGAC
 GTCTTCTCT CAGGCCCCC CHGACXCCC GTAGTCATG CCCCACACAG CCCCACCTTC TGCTCCCTG GGTTCCTG GCGGGGCC CACCCCGCTG
 201 TTGGGGGAG TTGGTGCCTC GCGCCCCAGG CTTTGGGCG GTCAUGGCG CCCCCCATTC TCGGGGCCCT GCTGGCTGCTG GCTGGCTGCTG
 AAACCCCTTC AACCAAGGG GCGGGGGTCC GGAACCTGCC CAGTACGCG CCGGGGTAAG ACCCGGCC CCGCAGCTC AGCCCGGCA CCGCAGCAG
 1 MetGlyP roProHisP GlyValArgV alGlyAlaLe uLeuLeuLeu
 301 CCGGTTTTGG GCTGTGCTG TCGGCTCAGC CTGGAGCCTG TCTACTGGA CTTGGGGAAT CCGGGCTTC AGCAGCAGGG TGCTTATGTG CTGTACCTTC
 CCCCCAAACC CCGACACACAG ACCCAGCTCC GACTCTGAG AGATGACTT GACCCGCTTA TTCTCCAAAG TGCTCTCTCC ACCAATAAC GACATCGGAG
 20 GlyValLeuG lylleuValse rGlyLeuSer LeuGluProV altyrTrpAs nSerAlaAsn LysArgPheG InAlaGluG lYglyTyrVal LeuTyrProGln
 401 AGATCGGGGA CCGGCTAGAC CTGCTCTGCC CCGGGGCCCG GCTCTCTGSC CCTCACCTCT CTCTTAATTA TGACTGTACT AAGCTGTACT TGCTTAATGCG
 TCTAGCCCCC TTAGCCCCC GCGCGATCTG CACGAGACCG GCGCGGGCG CCGAGGACCG GGACTGAGA GAGGATTAAT ACTCAAGATG TTGGACATCG ACCATCCCCC
 54 IloglyAs pArgGluAsp leuLeuCySP roArgAlaAr gProProGly ProHisSer erProAsnTy rGluPheTyr LysLeuTyrL cuValGlyGly
 501 TGCTCAGGG CCGCCCTGTG AGCACCCTCC TGCCCCAAAC CTCTTTCTCA CTTGTGATCG CCGGACCTTG GATCTCCCTT TCACCATCAA GTTCCAGGAC
 ACCAGTCTCC GCGCGGACAC TCGCTGGGG AGCGGTTTG GAGGAACAGT CAACACTTAC GGGTCTGAC ACTCAAGATG TTGGACATCG ACCATCCCCC
 8/ AlaGlnGly ArgArgCySG luAlaProPr oAlaProAsn LeuLeuLeuT hrcysAspAr gProAspLeu AspLeuArgp heuTrileLy spheGlnGlu
 601 TATAGACCTA ATCTCTGGG CCACGAGTTC CGCTCGCACC AUGATTTACTA CATCATTCGC ACATCGGAGT GCACCCGGGA GGGCTGGAG AGCTTCGACG
 ATATCGGAT TAGAGACCCC GGTGCTCAAG GCGAGCGTGG TGCTAATGAT GTAGTAACCG TCTACCCCTAC CCGGGCCCTT CCGGACCTTC TCGGAGCTCC
 120 TyrSerProA snLeuTrpG lylisGluPhe ArgSerHis h isAspTyrTy rIleIleAla ThrSerAspG lyThrArgG lYglyLeuGlu SerLeuGlnGly
 701 GAGGTGCTG CTTAACCAGA GGCATGAAG TCTTCTCCG ACTGGGACAA ACTCCCTCCG CAGGGGCTCT CCCCCGAAA CCGTGTGCTG AATTCCTCAT
 CTCCACACAC GGATTGCTT CCGTACTTCC ACCAGAGGC TCACTCTGTT TCAGGCGCTC CTCTCCGACA GGGGCTTTT GGACACAGAC TTATACGCTA
 154 GlyValCy sLeuThrArg GlyMetLysv alIleuLeuT hrcysAspAr gProArgG lYglyAlaVa lProArgLys ProValSerG luMetProMet
 801 GGAAGAGAC CAGGGGGCAG CCAACAGCTT GGAGCTTGG AAGGAGAACC TGCCAGCTCA CCCCACACG NATGCAACCT CCGGGGTTC TGAACGCTCC
 CTTTCTCTG CTTCCCTTC GGGTCTCGGA CTTCCCTTGG ACCGTCTACTT GAGGTGGTGG TTACTCTTGA GGGCCCCACG ACCTTCAGG
 187 GluArgAsp ArgGlyAlaAla lalisSerLe uGluProGly LysGluAsnL euproGlyAs pProHisSer AsnAlaThrS erArgGlyAla aGlnGlyPro
 901 CTTCCCTCTC CCAGCATGCC TGCAGTGGCT GGGGCTCTGG GCTGCTCTTC CTGGGCTTGG CAGGGGCTGG GGTCTCCATG TGTTGGCGGA
 GAGCGGGGAG GGTCTGACCG AGGTACGCA CCGGCTCTG CTTCCCTTGG ACCGTCTACTT GAGGTGGTGG TTACTCTTGA GGGCCCCACG ACCTTCAGG
 220 LeuProProp roSerMetPr oAlaValAla GlyAlaAlaC lYglyLeuAl aleuLeuLeu LeuGlyVala laGlyAlaG lYglyAlaMet. CysTrpArgArg
 1001 GACGGGAGGC CAAGCTTTC GAGAGTCTGC ACCCTGCTTC TGCTCTCTTC CCGAGGGGAG GGTCTCTTGG CTTGGGGGTG GGAGCTTGGG TGCGACCTTC
 CTGCCCCCTC GTTCGGAAG CTTCTACCTG TGGGACCAAG ACCGACCAAG CCGTCCCTTC CCGACACACC GGACCCCCCA CTTCCACCTT ACCCTGGACG
 254 ArgArgAl aLysProSer GluSerArgH isProGlyPr oglySerPhe GlyArgGlyG lySerLeuCl yLeuGlyGly GlyGlyGlyM etIlyProArg

FIGURE 2B

1101 GGAGGCTGAG CTTGGGGAGC TAGGAATAGC TCTGGGGGT GCGGGGGGTG CAGATCCCCC CTCTGCCCC CACTATGAGA AGTGAGTGG TGACTNKGCC
 287 CTTCCGACTC GGACCCCTCG ATCCCTATCG AGACGCCUCA CCGCCCGAC GTCTAGGGGG GAAGACGGGG GTGATACTCT "KCCACTCACC ACTGATACCC
 GluAlaGlu ProGlyGluL euGlyIleAl aLeuAlrGly GlyGlyAla laaspProPr oPheCysPro HisTyxGluL ysaIserGL yAspTyxGly
 1201 CATCCCTGTGT ATATCGTGA ATATCGTGA GATGGGCC CCCAGAGCCC CTCCAAACAT CTACTACAAG GTATGAGGGC TCCCTCAGC TGGCTATCTT CAATCCAGCC
 GTAGGACACA TATAGCAGGT CCTACCCGG GGGGTCTCG GAGGT"TGTA GATCATGTTC CATACTCCCG AGGAGAGTGC ACCGATAGGA CTTAGGTCCG
 320 HisProValT yIleValGL nAspGlyPro ProGlnSerP roProAsnII eTyTyxLys Valop*
 1301 CTTCTTGGGG TGTCTCTCCA GTTAAATTC TGGTTTGGG GACACCTCTA ACATCTCGG CCCCTGTGCC CCCCAGCCCC CTTCACCTCT CCCGGGTGCT
 GAAGAACCCC ACGAGGAGGT CAATTAAGG ACCAACTCC CTGTGGAGAT TGTAGAGCCG GCGCACACGG GCGGTCCGG GAAGTAGGA GGGCCGACGA
 1401 GTCTCTGCTT CCACPTTTAG GATTCCTTAG GATTCCTTAG GATTCCTTAG CCCCCACTT CCGCCCTCCC GTGCCCCCA" CCGTCCCCC CTCTCTCTCA GTGTCCCTGG
 CAGGAGCAGA GGTGAAAATC CTAAGGAATC CTAAGGTGA CCGGGTGAAG GACGGGAGGG CAACCCGTA CCAACCCGTA CCAACCCGTA CCAACCCGTA CCAACCCGTA
 1501 ATCCCTTTTC CTTGGGGAGG GGCACAGGCT CAGCCCTCTC ICTGACCATG ACCAGGCCAT CCTTGTCCC CCTTGTCCC CACAGCTAGG GCGGGGAACA
 TAGGAAAAG GAAACCCCTCC CCGTGTCCGA GTCCGAGGAG AGACTGGTAC TGGTCCGTA GGAACAGGGG GAGTGGGTGG GTCTCGATCC CCGCCCTGT
 1601 GCCCACCTTT TGGTGGCAC CCGCTTCTTT CTGCTCTCTCA CTGGT"TTCT CTTCCTCTATC TCTTATCTCT "KCCCTCTCTT CCGTCTCTAG GTCTGTCTT
 CCGGTGAAA ACCAACCGTG CCGGAAGAA GACGAGAGT GACCAAGA GAAGAGATG AGAATAGAA AGGAGAGAA AGGAGAGAA AGGAGAGAA AGGAGAGAA
 1701 CTTCCCTAGC ATCTCTCTCC CCACATCTCC TTCCACCTCT TTGGT"TTCT ATCTCTGTC TCTTCCCTCT CTTCCCTCTT CCGATCAAA CAFTTCTCCC
 GAAGGATAGC TAGGAGGAGG CCGTGTAGAG AAGTGGGAG AACCAAGAA TAGGACACGG AGAGGTAGA GACCCACACC CCTAGTTTC GTAAAGAGGG
 1801 CTTAGCTTTT AGCCCCCTT CTGACCTCTC ATACCAACCA CTCCCTCTAG TCTGCCAAA ATGGGGGCTT TATGGGMA GCTCTGACAC TCCACCCCAG
 GAATCGAAG TCGGGGGGA GACTGGAGG TATGGT"GGT" CAGGGGAGTC AGACGGT"TTT TACCCCCCGA ATACCCCTTC CGAGACTGTG AGGTGGGTTC
 1901 CTCAGGCCAT GGCAGCCAGG GCTCCATTTCT CTGGCTTGGC CCAGGCTCTT ACATCTTAC TCCAGCCAT TGGGTGGTT GGTCTNTGAC AGCTACCATG
 GAGTCCGGTA CCGTCTGCTC CGAGTAAGA GACCGGACCG GGTCCGAGA TGTATGAATG AGGTCCGTAA ACCCCACCAA CCGAGTACTG TCGATGGTAC
 2001 AGAAGAGTGT TCCCGTTTGT TCCAGTGGCC ATATGCAAGA TATCAACCGG TGGGACATG TATGGACTTG GTCTGNTCTT GAATGGGCA CT"TGGAACCG
 TCTTCTTCA AGGCCAAAAC AGGTCAACCG T"ATCGT"CT ATACTTGGCC AGCCCTGTAC ATACCTGAAC CAGACTAGA CTTACCCGGT GAACCTTGGC
 2101 GAAGTCACTT GCTCCAGACA AGAGGTGACC AGGCCCGGAC AGAATGGCC TGGGAAGTAG CAGAAGCACT GCAGCAGGAA CTGGAAGTGC CTTGATCCAG
 CTTCACTGAA CGAGGTCTGT TCTCCACTGG TCCGGGCTGT TCTTACCGC ACCCTTCAVC GTCTTGGTCA CGTCTCTCTT GACCTTCACG GAAGTAGCTC
 2201 GACAGGAAGT AGCATTTCTG NAACAGGAAG TGGTCTGGCT GGAACCTCAA GTGGCTTAGT CTGGGGGATC AGGAGGTGG AGGTGGNTGG TCTTATTCTT
 CTCTCTTCA TCGTGAAGAC TTTGTCTTTC ACCAGACCGA CCTTCAGGTT CACCGAATCA GACCCCTAG TCTTCCAGCC TCCACCTACC AAGAATAGA
 2301 GTGAGAGA AGGGCGGGA GAACCTTCTT TCAGGACGAA CCTTGAACCTT ACTGACTGTA AGAGTTTACA CGTGGACCGA CCGTGGACCTT
 CACCTCTCTT TCCCGGCTT CT"TGAAAGAA AGTCTCTCTT CGACCTTGAA TGAATGACAT TCTCCAATCT CCACCTGGCT

[illegible]

AL-2b.L 1 C T C T A C A A N T A G T G S A T C C C C C G G G C T G C A G S A T T T C G A C S S C C C C T

AL-2b.L 51 G 3 A A S G G G C T C T G G T G G G G C T G A G C G C T C T G C C G G G G G G G G C C C C A D A G

AL-2b.L 101 C A G G A A G C A G G T C C G C G T G G G C G C T G G G G G C A T C A G C T A C C S S G G T G G T C

AL-2b.L 151 C G G G C T G A A G A G C C A S G C A G C C A A G G C A G C C A C C C C S G G G G T S G C C G A C

AL-2b.L 201 T T T G G G G G A G T T G S T G C C C C G C C C C C A G G G C T T G S G G G G T C A T G S S G C

AL-2b.L 251 C C C C C C A T T C T S S G C C G G G G G G C G T G C G A G T C C G G G C C C T G C T G C T G C T G

AL-2b.L 301 G G G G T T T T G G S G C T G T G T C T G G G C T C A G C C T G G A G C C T G T C T A C T G G A A

AL-2b.L 351 C T C G G C G A A T A A G A G G T T C C A G G C A G A G G G T G G T T A T C T G C T G T A C C C T C

AL-2b.L 401 A G A T C G G G G A C C G G C T A G A C C T G C T C T G C C C C C G C C C C G G G C T C C T G C C

AL-2b.L 451 C C T C A C T C C T C T C C T A A T T A T G A G T T C T A C A A G C T G T A C C T G G T A G G G G G

AL-2b.L 501 T G C T C A G G G G C C G C G T G A G G C C C C T G C C C C A A A C C T C C T T C T C A
H10006 1 G C C G A C G C T G T G A G G G C A C C C C T G C C C C A A A C C T C C T T C T C A

AL-2b.L 551 C T T G T G A T C G C C C A G A C C T G G A T C T C C G C T T C A C C A T C A A S T T C C A G G A G
H10006 43 C T T G T G A T C G C C C A G A C C T G G A T C T C C G C T T C A C C A T C A A G T T C C A G G A G

AL-2b.L 601 T A T A G C C C T A A T C T C T G G G G C C A C G A B T T C C G C T C G C A C C A C G A T T A C T A
H10006 93 T A T A G C C C T A A T C T C T G G G G C C A C G A B T T C C G C T C C C A C C A C G A T T A C T A

AL-2b.L 651 C A T C A T T G C C A C A T C G G A T S S G A C C C G G G A G G G C T G G A G A G C C T G C A G G
H10006 142 C A T C A T T G C C A C A T C G G A T S S G A C C C G G G A G G G C T G G G A G A G C C T G C A G G

AL-2b.L 701 G A G G T G T G T G C C T A A C C A G A S C A T G A A G S T G C T T C T C C G A G T G G G A C A A
H10006 252 G A A G T G T C T G C C T A A C C A G A G S C A T G A A C S T G C T T C T C C G A G T N G G A C A A

AL-2b.L 751 A G T C C C C G A G G A G G G G C T G T C C C C C G A A A A C C T G T C T G A A A T G C C C A T
H10006 243 A G T C C C C G A G G A G G G G C T G T C C C C C G A A A A C C T G T C T G A A A T G C C C A T

AL-2b.L 801 G G A A A G A G A C C G A G G G G C A G C C C A C A G C C T G G A G C C T G G G A A G C A G A A
H10006 292 G C A A A G A G A C C G A G G G G C A G C C C A C A G C C T G G G A G C C T G G G A A G G A G A A

AL-2b.L 849 C C T G C C A G G T G A C C C C A C C A G C A A T G S A A C C T C C C G G G T C C T G A A G G
H10006 312 C C T G C C A G G T G A C C C C A C C A G C A A T N C A A C C T C C G S G G T T C C T G A A G G

AL-2b.L 907 C C C C C T G C C C C C C C A G C A T T G C C T G C A G T G G C T G G G C A G C A G G
H10006 352 C C C C C T G A C C C T T C C C A G C A T T G C A T G C A N T T G G T T G G G C A G C A N G

AL-2b.L 947 G G G G C . . . T G G C G C T G C T T G C T G G G C T G G G A G S S G C T G G S G G T C C
H10006 441 G G G G C T T T T G G C

AL-2b.L 998 A T G T G T T G C G G G A G A G G G C G G G C A A G C C T T C G G A G A G T C G C C A C C C T G G

AL-2b.L 1008 T C C T G G C T C C T C G S G A G G G A G G G T C T C T G G G C C T G G G G S S T G S A G G T G

AL-2b.L 1088 G G A T C G G A C C T C G G C T G A G C C T C C C A G G T A G G C A T A G C T G C C G C

AL-2b.L 1108 G G T G S C G G G G C T G C A C A T C C C C C T T C T S C C C C A C A T A T G A G A A G G T G A G

AL-2b.L 1195 YGGTGACTATG CATCCGTGTGTATACTGCGAGGATGGG JCCCCCAGA

AL-2b.L 1235 GCGCTCCAAACATCTACTACAGATCGATTCTGTETGGAGTGGCCCATATA

AL-2b.L 1275 TTGCATACGATACAACTGTCTTCACTGGATCCAAAGTGGTCCCGGTGTCAAC

AL-2b.L 1315 TACATTCTTATTCTGTGTGCAAGTATTATAGGACATCGACTTGGCGGATGA

AL-2b.L 1355 CTTCATTTAGCTTTACGAGCGCTGAACCCATCCATGCCAGGCGTGCAGAGCA

AL-2b.L 1405 CAGATGGGGGAATTCCGATATCAGATGGGTGTCTGGGGGGACAGGATCCT

AL-2b.L 1445 GGGTACGGCTCTGTGTGTCTTGTGCTTATTCTCTCTTGGGAGCGCTGA

AL-2b.L 1535 ATATGCATCAGACGACACTGCTCCGGCAACGGGCCAGTGTGAGGCGGAA

AL-2b.L 1585 GCGGCCCCAGCATGGTCCCGCTGTGATAGGATTGAAGAGCTACTGAGATTA

AL-2b.L 1635 GGGGCGTTCTCAATCAGAGAGCGCGAGGCTGCTGTATCATGGGAACCAAGG

AL-2b.L 1685 CAGATCAATCACTCCCTGGCAGGTACAGGCAAGGAAGTTACTTAGCTTCTCCT

AL-2b.L 1735 TCACCTCTCTCCACAGGAATTTATTAAGGCTTGTTCCAAGTGTAGTGT

AL-2b.L 1785 GTGATCAGATTCTGCTGCTGTGCTACCTGGCACTTCCCC

AL-2b.L 1835 TCAAGGAATTCGATATCAAGCTTATCGATACCGTCCACCT

FIGURE 3B

LERK2.1 1 MA- R P G Q R W L G K W L V A M V V W A L C R L A T P L A K N L E P V S W S S L N P K F L S G K G
huHTKL 1 M A V R R D S V W K Y C W G V L M Y - - - L C R T A I S K S I V L E P I Y W N S S N S K F L P G G G
ALII.long 1 M G P P H S G P - G G Y R V G A L L L - - - L G V L G L V S G L S L E P V Y W N S A N K R F Q A E G G

LERK2.1 50 L V I Y P K I G D K L D I I C P R A - - - E A G R - - - P Y E Y K L Y L V R P E Q A A A C S T V L D
huHTKL 48 L V L Y P Q I G D K L D I I C P K V - - - D S K T V G O Y E Y K V Y M Y D K D Q A D R C T I K K E
ALII.long 48 Y V L Y P Q I G D R L D L L C P R A R P P G P H S S P N Y E F Y K L Y L V G G A Q G R R C E A P P A

LERK2.1 95 P N V L V T C N R P E Q E I R F T I K F Q E F S P N Y M G L E F K K H H D Y Y I T S T S N G S L E G
huHTKL 95 N T P L L N C A K P D Q D I K F T I K F Q E F S P N L W G L E F Q K N K D Y Y I I S T S N G S L E G
ALII.long 98 P N L L L T C D R P D L D L R F T I K F Q E Y S P N L W G H E F R S H H D Y Y I I A T S D G T R E G

LERK2.1 145 L E N R E G G V C R T R T M K I I M K V G O D P N A V T P E O L T T S R P S K E A D N T V K M A T O
huHTKL 145 L D N Q E G G V C O T R A M K I L M K V G O D A S S - - - - - A G S T R N K D P T R R P E L E A G
ALII.long 148 L E S L O G G V C L T R G M K V L L R V G O S P R - - - - - G G A V P R K P V S E M P M E - R

LERK2.1 195 A P G S R G S L G D S D G K H E T Y N Q E E K S G P G A S G G S S G D P D G F F N S K V A L F A A V
huHTKL 189 T N G - R S S T T S P F V K P N P G S S T D G N S A G H S G - - - - - N N I L G S E V A L F A G I
ALII.long 189 D R G A A H S L E P G K E N L P G D P T S N A T S R G A E G - - - - - P L P P P S M P A V A G A

LERK2.1 245 G A G C V I F L L I I I F L T V L L L K L R K R H R K H T O R A A A L S L - - - S T L A S P K G G
huHTKL 232 A S G C I I F I V I I I T L V V L L L K Y R R R H R K H S P Q H T T T L S L - - - S T L A T P K R S
ALII.long 232 A G G L A L L L L G V A G A G G A M C W R R R R A K P S E S R H P G P G S F G R G G S L G L G G G G

LERK2.1 292 S - G T A G T E P S D I I I P L R - - - T E N N Y C P H Y E K V S G D Y G H P V Y I V O E M P P O
huHTKL 279 G - N N N G S E P S D I I I P L R - - - T A D S V F C P H Y E K V S G D Y G H P V Y I V O E M P P O
ALII.long 282 G M G P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G D Y G H P V Y I V O D G P P O

LERK2.1 338 S P A N I Y Y - - - - -
huHTKL 325 S P A N I Y Y - - - - -
ALII.long 332 S P P N I Y Y T S I S V L E W P I L H T I O L F F M R S K C S R V T T F L P P V O V I T T S T C R M

LERK2.1 345 - - - - - K V - - - - -
huHTKL 332 - - - - - K V - - - - -
ALII.long 382 T S F S F T T L N P S M Q A C R A O M G E F R I R W C F W G D R I L G T A L F V L V L I L L L G R L

ALII.long 432 N M H O T T L L R O R A S V E A E A G O H G P L

FIGURE 5